

REMARKS

Claims 1, 85, and 92 have been amended for greater clarity. The amendments are fully supported by the original specification (see, e.g., page 10, lines 11-13; page 18, lines 6-14; page 19, lines 10-17; Figures 5A, 6A, 6B; Table 1 on page 9; and Example 1 on pages 17-22). No new matter has been introduced. The amendments are made solely to expedite prosecution of the application, and Applicants reserve the right to prosecute claims of similar or differing scope in subsequent applications.

Applicants respectfully request reconsideration in view of the following remarks. Issues raised by the Examiner will be addressed below in the order they appear in the Office Action.

Applicants note that the Amendments filed on November 26, 2004 have been entered in full.

Applicants further note that the previous rejections under 35 U.S.C. § 102(b) (citing Hornes et al.) and under 35 U.S.C. § 102(e) (citing Zhu et al.) have been withdrawn in view of Applicants' Amendments and Response filed on November 26, 2004. However, the Examiner has cited new art in this Office Action.

Objection to Drawings

The Examiner has objected to the drawings as being informal. In response, Applicants enclose herewith formal drawings. Reconsideration and withdrawal of this objection is respectfully requested.

Claim Rejections under 35 U.S.C. § 102(b)

Claims 1-6, 73, 85-87, 90-92, and 95-96 are rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Kohno et al. (Gene 188: 175-181, 1997). Applicants respectfully traverse this rejection.

First, the Office Action asserts that "[t]he following rejection is based upon the following interpretation of the term 'mRNA encoding at least a portion of an antibody,' or variations thereof (i.e., framework or constant regions) used throughout claims 4, 85-87 and 92. The term 'mRNA encoding at least a portion of an antibody' is very broad in scope because a single

amino acid residue can represent a “portion of an antibody” (see Office Action, page 3, lines 17-22).

Applicants respectfully traverse the Examiner’s claim construction of the term “at least a portion.” Applicants submit that the specification teaches features of the claimed plasmids. For example, the specification teaches that [t]he downstream primer and upstream collar sequence should be of **sufficient length** to support specific and stable hybridization to the target complementary mRNA. The annealing sequences may individually contain from about 10 nucleotides to about 50 or more nucleotides in length. Preferably, the individual annealing sequences are 15 to 35 nucleotides in length” (see e.g., page 6, lines 18-22, emphasis). In view of the teachings of the specification one of ordinary skill in the art, would not construe the claims as the Examiner suggests, but rather, the skilled artisan would know the metes and bounds of the term “at least a portion.” Further, Applicants wish to draw the Examiner’s attention to a recent Federal Circuit decision *Phillips v. AWH Corp.*, 2005 WL 1620331 (Fed. Cir. July 12, 2005). In this opinion, the *en banc* majority holds that when construing patent claims, a court should **consult the specification** and prosecution history to determine if the patentee intended to use particular terms in ways other than their ordinary meaning. Thus, Applicants respectfully submit that the Examiner’s claim construction is not consistent with the teachings of the specification.

Second, the Office Action asserts that “the plasmid of Figure 1B [in Kohno] has a 5’ ‘primer’ sequence capable of binding to a first portion of a nucleic acid encoding the polypeptide known as Rad52. Kohno also teaches a 3’ ‘collar’ sequence that is capable of binding to a second portion of a nucleic acid sequence encoding Rad52, wherein **the ‘primer’ and ‘collar’ sequences are separated by at least 20 nucleotides long**; this is evident from the presence of HIS5 gene . . .” (see Office Action, page 4, lines 11-16, emphasis added).

Applicants respectfully disagree. However, solely in an effort to expedite prosecution, Applicants have amended independent claim 1 to clarify that the primer sequence and the collar sequence adjoin one another to create at least one restriction site. Support for the amendments can be found throughout the original specification (see, e.g., page 10, lines 11-13; page 18, lines 6-14; page 19, lines 10-17; and Figures 5A, 6A, and 6B). Applicants have further amended claims 85 and 92 to specify the “framework region” associated with the antibody. Support for

the amendments can be found throughout the original specification (e.g., Table 1 on page 9; and Example 1 on pages 17-22).

Applicants respectfully submit that the Office Action mischaracterizes the claimed subject matter. Claim 1 recites that the **second portion** of the polypeptide encoding portion of the nucleic acid is separated by at least 20 nucleotides from the **first portion** of the polypeptide encoding portion of the nucleic acid. However, the Office Action incorrectly construes that the **primer sequence** and the **collar sequence** are separated by at least 20 nucleotides. As a matter of fact, the amended claims specify that the primer sequence and the collar sequence adjoin one another to create at least one restriction site.

The standard for anticipating a claim is clearly outlined in MPEP 2131, and this standard is further supported by the Courts. “A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference.” *Verdegaal Bros. v. Union Oil Co. of California*, 814 F.2d 628, 631 (Fed. Cir. 1978).

Applicants contend that Kohno et al. fail to satisfy this criteria for anticipating the present invention. Kohno et al. describe a “pMWrad” plasmid for disrupting yeast Rad52 gene (see e.g., page 177, Figure 1B). This pMWrad plasmid contains a HIS5 gene flanked by a downstream nucleic acid sequence encoding a first portion of Rad52 and an upstream nucleic acid sequence encoding a second portion of Rad52. As noted in the Office Action, the HIS5 gene is 1158-nucleotide long (Office Action, page 4, line 16). Thus, the downstream nucleic acid sequence (proposed to be the “collar sequence” by the Office Action) is **separated** from the upstream nucleic acid sequence (proposed to be the “primer sequence” by the Office Action) **by at least 1158 nucleotides** (i.e., the HIS5 gene).

Accordingly, Kohno et al. fail to anticipate independent claim 1 because Kohno et al. do not teach or suggest that the primer sequence and the collar sequence adjoin one another to create at least one restriction site as recited in amended claim 1. For the same reasons, Applicants submit that all claims depending from claim 1 are not anticipated by Kohno et al.

In addition, Kohno et al. fail to anticipate independent claims 85 and 92 because Kohno et al. simply fail to teach or suggest the coding sequence of the mRNA encoding the framework

region associated with the antibody or the constant region associated with the antibody as recited in claims 85 and 92. For the same reasons, Applicants submit that all claims depending from claims 85 and 92 are not anticipated by Kohno et al.

In view of the above amendments and arguments, Applicants respectfully request reconsideration and withdrawal of this rejection under 35 U.S.C. § 102(b).

Allowable Subject Matter

Applicants note with appreciation that claims 23, 24, 26-37, and 74 have been allowed.

CONCLUSION

For the foregoing reasons, Applicants respectfully request reconsideration and withdrawal of the pending rejections. Applicants believe that the claims are now in condition for allowance and early notification to this effect is earnestly solicited. Any questions arising from this submission may be directed to the undersigned at (617) 951-7000. If an addition fee is due, please charge our Deposit Account No. 18-1945, under Order No. ALEX-P01-055 from which the undersigned is authorized to draw.

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Respectfully submitted,

By Anita Varma
Anita Varma

Registration No.: 43,221
ROPES & GRAY LLP
One International Place
Boston, Massachusetts 02110-2624

(617) 951-7000
(617) 951-7050 (Fax)
Attorneys/Agents For Applicant